



SEQUENCE LISTING

<110> Madison, Edgar
Ong, Edgar
Yeh, Juinn-Chern

<120> NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE 16, THE
ENCODED PROTEINS AND METHODS BASED THEREON

<130> 24745-1625

<140> 10/612,466

<141> 2003-07-01

<150> 60/394,347

<151> 2002-07-02

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<170> FastSEQ for Windows Version 4.0

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<211> 3147

<212> DNA

<213> Homo Sapien

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<221> CDS

<222> (23)...(2589)

<223> Nucleotide sequence encoding MTSP1

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<308> GenBank #AR081724

<309> 2000-08-31

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Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn
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Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
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Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	
765	770
ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc	2404
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 <212> DNA
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<220>
 <221> CDS
 <222> (1865)...(2590)
 <223> Nucleic acid sequence of protease domain of MTSP1

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tcgt gtt gtt ggg ggc acg gat gcg		gat gag ggc		gag tgg ccc tgg cag		1909
Val Val Gly Gly Thr Asp Ala	Asp Glu Gly Glu Trp Pro Trp Gln					
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Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp	
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Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly	
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ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg	2101
Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg	
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Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp	
80 85 90 95	
tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc	2197
Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser	
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Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala	
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Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly	
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Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met	
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Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser	
180 185 190	
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Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala	
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Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly	
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Gly Val *	
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Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
 35      40      45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
 50      55      60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
 65      70      75
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
 85      90      95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100      105      110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115      120      125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130      135      140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145      150      155
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165      170      175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180      185      190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195      200      205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
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Val

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 1      5      10      15

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cct gaa gat ctg gac tgc ggg cgc cct gag ccc tcg gcc cgc atc gtg Pro Glu Asp Leu Asp Cys Gly Arg Pro Glu Pro Ser Ala Arg Ile Val 35 40 45	144
ggg ggc tca aac gcg cag ccg ggc acc tgg cct tgg caa gtg agc ctg Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu 50 55 60	192
cac cat gga ggt ggc cac atc tgc ggg ggc tcc ctc atc gcc ccc tcc His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser 65 70 75 80	240
tgg gtc ctc tcc gcc gct cac tgt ttc atg acg aat ggg acg ctg gag Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu 85 90 95	288
ccc gcg gcc gag tgg tcg gta ctg ctg ggc gtg cac tcc cag gac ggg Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly 100 105 110	336
ccc ctg gac ggc gcg cac acc cgc gca gtg gcc gcc atc gtg gtg ccg Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro 115 120 125	384
gcc aac tac agc caa gtg gag ctg ggc gcc gac ctg gcc ctg ctg cgc Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg 130 135 140	432
ctg gcc tca ccc gcc agc ctg ggc ccc gcc gtg tgg cct gtc tgc ctg Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu 145 150 155 160	480
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ggc tgg gga gac gtc cag gag gca gat cct ctg cct ctc ccc tgg gtg Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val 180 185 190	576
cta cag gaa gtg gag cta agg ctg ctg ggc gag gcc acc tgt caa tgt Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys 195 200 205	624
ctc tac agc cag ccc ggt ccc ttc aac ctc act ctc cag ata ttg cca Leu Tyr Ser Gln Pro Gly Pro Phe Asn Leu Thr Leu Gln Ile Leu Pro 210 215 220	672
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Pro	Gly	Val	Phe	Thr	Ala	Val	Ala	Thr	Tyr	Glu	Ala	Trp	Ile	Arg	Glu		
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Gln	Val	Met	Gly	Ser	Glu	Pro	Gly	Pro	Ala	Phe	Pro	Thr	Gln	Pro	Gln		
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Lys	Thr	Gln	Ser	Asp	Pro	Gln	Glu	Pro	Arg	Glu	Glu	Asn	Cys	Thr	Ile		
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gcc	ctg	cct	gag	tgc	ggg	aag	gcc	ccg	cgg	cca	ggg	gcc	tgg	ccc	tgg	1008	
Ala	Leu	Pro	Glu	Cys	Gly	Lys	Ala	Pro	Arg	Pro	Gly	Ala	Trp	Pro	Trp		
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Glu	Ala	Gln	Val	Met	Val	Pro	Gly	Ser	Arg	Pro	Cys	His	Gly	Ala	Leu		
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Val	Ser	Glu	Ser	Trp	Val	Leu	Ala	Pro	Ala	Ser	Cys	Phe	Leu	Asp	Pro		
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aac	agc	tcc	gac	agc	cca	ccc	cgc	gac	ctc	gac	gcc	tgg	cgc	gtg	ctg	1152	
Asn	Ser	Ser	Asp	Ser	Pro	Pro	Arg	Asp	Leu	Asp	Ala	Trp	Arg	Val	Leu		
		370					375				380						
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Leu	Pro	Ser	His	Pro	Arg	Ala	Glu	Arg	Val	Ala	Arg	Leu	Val	Gln	His		
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gag	aac	gct	tgc	tgg	gac	aac	gcc	ccg	gac	ctg	gcg	ctg	ctg	cag	ctg	1248	
Glu	Asn	Ala	Ser	Trp	Asp	Asn	Ala	Pro	Asp	Leu	Ala	Leu	Leu	Gln	Leu		
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cgc	acg	ccc	gtg	aac	ctg	agt	gcg	gct	tgc	cgg	ccc	gtg	tgc	cta	ccc	1296	
Arg	Thr	Pro	Val	Asn	Leu	Ser	Ala	Ala	Ser	Arg	Pro	Val	Cys	Leu	Pro		
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cac	ccg	gaa	cac	tac	ttc	ctg	ccc	ggg	agc	cgc	tgc	cgc	ctg	gcc	cgc	1344	
His	Pro	Glu	His	Tyr	Phe	Leu	Pro	Gly	Ser	Arg	Cys	Arg	Leu	Ala	Arg		
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tgg	ggc	cgc	ggg	gaa	ccc	gcg	ctt	ggc	cca	ggc	gcg	ctg	ctg	gag	gcg	1392	
Trp	Gly	Arg	Gly	Glu	Pro	Ala	Leu	Gly	Pro	Gly	Ala	Leu	Leu	Glu	Ala		
		450				455					460						
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Glu	Leu	Leu	Gly	Gly	Trp	Trp	Cys	His	Cys	Leu	Tyr	Gly	Arg	Gln	Gly		
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gcg	gca	gta	ccg	ctg	ccc	gga	gac	ccg	ccg	cac	gcg	ctc	tgc	cct	gcc	1488	
Ala	Ala	Val	Pro	Leu	Pro	Gly	Asp	Pro	Pro	His	Ala	Leu	Cys	Pro	Ala		
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tac	cag	gaa	aag	gag	gag	gtg	ggc	agc	tgc	tgg	aat	gac	tgc	cgt	tgg	1536	
Tyr	Gln	Glu	Lys	Glu	Glu	Val	Gly	Ser	Cys	Trp	Asn	Asp	Ser	Arg	Trp		

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Ser Leu Leu Cys Gln Glu Glu Gly Thr Trp Phe Leu Ala Gly Ile Arg															
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gac ttt ccc agt ggc tgt cta cgt ccc cga gcc ttc ttc cct ctg cag	1632														
Asp Phe Pro Ser Gly Cys Leu Arg Pro Arg Ala Phe Phe Pro Leu Gln															
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Thr His Gly Pro Trp Ile Ser His Val Thr Arg Gly Ala Tyr Leu Glu															
545	550														
gac cag cta gcc tgg gac tgg ggc cct gat ggg gag gag act gag aca	1728														
Asp Gln Leu Ala Trp Asp Trp Gly Pro Asp Gly Glu Glu Thr Glu Thr															
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Glu Ala Ala Pro Val Gly Val Leu Trp Pro Trp Leu Ala Glu Val His															
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Val Leu Ala Ala Thr His Cys Val Leu Arg Pro Gly Ser Thr Thr Val															
625	630														
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Pro Tyr Ile Glu Val Tyr Leu Gly Arg Ala Gly Ala Ser Ser Leu Pro															
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Gln Gly His Gln Met Thr Ser Ala Pro Pro Leu Leu Cys Gln Met Thr															
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Pro His Ala Val Tyr Phe Leu Leu Leu Leu Thr Leu Leu Ile Gln Ser															
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2293

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<212> PRT
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Gly Gly Ser Asn Ala Gln Pro Gly Thr Trp Pro Trp Gln Val Ser Leu
50 55 60
His His Gly Gly Gly His Ile Cys Gly Gly Ser Leu Ile Ala Pro Ser
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Trp Val Leu Ser Ala Ala His Cys Phe Met Thr Asn Gly Thr Leu Glu
85 90 95
Pro Ala Ala Glu Trp Ser Val Leu Leu Gly Val His Ser Gln Asp Gly
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Pro Leu Asp Gly Ala His Thr Arg Ala Val Ala Ala Ile Val Val Pro
115 120 125
Ala Asn Tyr Ser Gln Val Glu Leu Gly Ala Asp Leu Ala Leu Leu Arg
130 135 140
Leu Ala Ser Pro Ala Ser Leu Gly Pro Ala Val Trp Pro Val Cys Leu
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Pro Arg Ala Ser His Arg Phe Val His Gly Thr Ala Cys Trp Ala Thr
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Gly Trp Gly Asp Val Gln Glu Ala Asp Pro Leu Pro Leu Pro Trp Val
180 185 190
Leu Gln Glu Val Glu Leu Arg Leu Leu Gly Glu Ala Thr Cys Gln Cys
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Leu Tyr Ser Gln Pro Gly Pro Phe Asn Leu Thr Leu Gln Ile Leu Pro
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Gly Met Leu Cys Ala Gly Tyr Pro Gly Gly Arg Arg Asp Thr Cys Gln
225 230 235 240
Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Gly Gly Arg Trp Phe
245 250 255
Gln Ala Gly Ile Thr Ser Phe Gly Phe Gly Cys Gly Arg Arg Asn Arg
260 265 270
Pro Gly Val Phe Thr Ala Val Ala Thr Tyr Glu Ala Trp Ile Arg Glu
275 280 285
Gln Val Met Gly Ser Glu Pro Gly Pro Ala Phe Pro Thr Gln Pro Gln
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Lys Thr Gln Ser Asp Pro Gln Glu Pro Arg Glu Glu Asn Cys Thr Ile
305 310 315 320
Ala Leu Pro Glu Cys Gly Lys Ala Pro Arg Pro Gly Ala Trp Pro Trp
325 330 335
Glu Ala Gln Val Met Val Pro Gly Ser Arg Pro Cys His Gly Ala Leu
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Val Ser Glu Ser Trp Val Leu Ala Pro Ala Ser Cys Phe Leu Asp Pro
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Thr	His	Gly	Pro	Trp	Ile	Ser	His	Val	Thr	Arg	Gly	Ala	Tyr	Leu	Glu
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Pro	Tyr	Ile	Glu	Val	Tyr	Leu	Gly	Arg	Ala	Gly	Ala	Ser	Ser	Leu	Pro
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Glu	Gly	Ser	Trp	Ile	Leu	Val	Gly	Met	Ala	Val	Gln	Gly	Ser	Arg	Glu
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Gly	Glu	Ala	Asn	Phe	Leu	Pro	Pro	Ser	Gly	Ser	Pro	His	Trp	Pro	Thr
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Gly	Gly	Ser	Asn	Leu	Cys	Pro	Pro	Glu	Leu	Ala	Lys	Ala	Ser	Gly	Ser
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 35 40 45

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<212> PRT

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<223> Polypeptide

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□